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RESULT 1
US-09-817-198A-2
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Sequence 701, App
Sequence 4, Appli
Sequence 1120, Ap
Sequence 2229, Ap
Sequence 2286, Ap
Sequence 2465, Ap
Sequence 2465, Ap
Sequence 534, App
Sequence 534, App
Sequence 534, App
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1087.611 Million cell updates/sec
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5 US-10-363-616-319 A3A

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                      December 25, 2004, 05:54:17
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   OM protein - protein search, using sw model
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RESULT 1

US-09-817-198A-2

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Patent No. US20020146758A1

GENERAL INFORMATION: US. Jane et al.

TITLE OF INVENTION: USCLATED HUMAN RAS-LIKE PROTEINS,

TITLE OF INVENTION: USCLATED HUMAN RAS-LIKE PROTEINS,

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

TITLE OF INVENTION: DROIS: 3010-103-27

UNDMER OF SEQ ID NOS: 33 2011-03-27

NUMBER OF SEQ ID NOS: 33 2011-03-27

NUMBER OF SEQ ID NOS: 33 2011-03-27

NUMBER OF SEQ ID NOS: 33 3011-03-27

USCANISM: Human

US-09-817-198A-2

OUGLY MATCH

Beet Local Similarity 100.0%; Score 1105; DB 9; Length 212;

Beet Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;

MAKCYPULFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKWKTIEVDGIKVRIQ 60

ON MAKCYPULFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKWKTIEVDGIKVRIQ 60

ON MAKCYPULFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKWKTIEVDGIKVRIG 60

ON HARCYPULFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKWKTIEVDGIKVRIG 60

ON HARCYPULFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKWKTIEVDGIKVRIG 60

ON HARCYPULFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKWKTIEVDGIKVRIG 60

ON GI IWDTAGGERYOTITKQYYRRAQGIFLVYDISSERSYQHIMKWWSDVDEFABEGVQKILG 120

ON GI IWDTAGGERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWWSDVDEFABEGVQKILG 120

ON GI IWDTAGGERYQTITKQYYRRAQGIFLVYDISSERSYCHIMKWWSDVDEFABEGVQKILG 120

ON GI IWDTAGGERYQTITKQYYRRAQGIFLVYDISSERSYCHIMKWWSDVDEFABEGVQKILG 120

ON GI IWDTAGGERYQTITKQYYRRAQGIFLVYDISSERSYCHIMKWSDVDEFABEGT 180

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Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT23
CURRENT PELICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper:
NUMBER OF SEQ ID NOS: 1510
SOFTWARR: Patentin Ver. 2.0
SSEQ ID NO 701
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                                                                                                                                                             APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
TILE REFERENCE: 21272-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
SEQ ID NO 319
                   181 RMRASNELALAELEEEEGKPEGPANSSKTCWC 212
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Publication No. US20040044181A1
GENERAL INFORMATION:
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Matches 212; Conservative
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Best Local Similarity 100.0
Matches 212; Conservative
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ORGANISM: Homo sapiens
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US-09-764-868-701
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61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120

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121 NKADEBOKROVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
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Betant No. US20020146758A1

GENERAL INFORMATION:

APPLICANT: YE, Jane et al.

TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/817,198A

CURRENT APPLICATION NUMBER: US/09/817,198A

CURRENT APPLICATION NUMBER: US/09/817,198A

SOFTWARE: PARLES OF IN NOS: 33

SOFTWARE: PARLES OF OF Windows Version 4.0
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Patent No. US20020146758A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
FILE REFERENCE: CL001188
CURRENT FILING DATE: 2010-03-27

NUMBER OF SEQ ID NOS: 33
SOFTWARE: PASSEQ for Windows Version 4.0

ELENGTH: 212
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; ORGANISM: Rattus norvegicus
US-09-817-198A-4
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TYPE: PRT
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Sequence 4, Appl
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(without alignments)
106.511 Million cell updates/sec
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Sequence 51,
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Sequence 10,
Sequence 34,
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Sequence 8, Al
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Sequence 49,
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1105
1 MAKQYDVLFRLLLIGDSGVG......LEBEBGKPEGPANSSKTCWC 212
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Sequence 3
Sequence 3
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-198-1184-4
US-08-511-255-25
US-08-511-255-51
US-08-511-255-51
US-08-511-255-51
US-08-511-255-51
US-08-511-255-51
US-08-511-255-10
US-08-511-255-10
US-08-511-255-10
US-08-511-255-10
US-08-718-270A-10
US-08-718-270A-14
US-08-916-901-3
US-09-154-602-3
US-09-154-602-8
US-09-118-25-14
US-08-511-525-13
US-08-511-525-13
US-08-214-33
                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                               478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                               December 25, 2004, 05:19:28
                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                - protein search, using sw model
                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                             Title:
Perfect score:
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Appli Appl 812, Appl Appl Appl 75, Ap 712, Ap 712, Ap 712, Ap 713, A Appl Appl Appli			0,
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Sequence Seq			, 0
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US-09-255-920A-7 US-08-511-255-19 US-08-718-270A-19 US-08-718-270A-19 US-09-255-920A-11 US-09-255-920A-11 US-09-255-920A-11 US-09-255-920A-11 US-09-270-767-48029 US-09-270-614-67 US-09-38-184-873-1 US-09-188-184-1 US-08-531-525-18		0	; 43;
9200A- 5525-1 7670-6- 9200A- 9200A- 767-8- 9134-6- 873-1 2700A- 2	TS	; 'n	, DB 2 3e-52; thes
2555 2555 2555 2555 2555 2555 2555 255	ALIGNMENT	, , se i	re 545; D d. No. 3e- Mismatches
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		T 1 -824-873-4 uence 4, Application US/08824873 uence 4, Application US/08824873 uence No. 2843717 APPLICANT: Hillman, Jennifer L. APPLICANT: Guegler, Karl TITLE OF INVENTION: 4 CORRESPONDENCE ADDRESS: 4 CORRESPONDENCE ADDRESS: 1 CORRESPONDENCE ADDRESS: 3 COUNTRY: DALO Alto STREET: 3174 Porter Drive STREET: 3174 Porter Drive CONFUTE: DALO Alto STREET: DALO ALTO STREET: DALO ALTO COMPUTER READBLE FORM: MEDIUM TYPE: Diskette COMPUTER READBLE FORM: MEDIUM TYPE: Diskette COMPUTER READBLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEO for Windows CUMPUTER: IBM Compatible OPERATING DATE: Filed Herewith FILING DATE: Filed Herewith FILING DATE: RIGH HERWITON: RAPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: BY-03 FILING DATE: REGISTRATION NUMBER: 36,749 REGISTRATION NUMBER: 36,749 REGISTRATION INFORMATION: TELEPONT AT 10 NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 207 amino acids TYPE: amino acid TYPE: LING ADENCE: LENGTH: SOURCE: LENGTH: SOURCE: LINMEDIATE SOURC	41
0 0		US/08824 Jennifer Karl A 4 18: Rarl Bis: Control Ratible Ratible Ratible Ratible Ratible Ratible Ratible Ration: Control Ration Ration: Control Ration: Contro	9.3%; 2.9%; ve
190 218 2218 2217 202 202 217 217 217 217 212 212 212 212 212 21		M: man, Jennife man, Jennife lier, Karl ON: NOVEL F CCES: 4 CDERSS: 4 CDERSS: 4 CDERSS: 4 CDERSS: 6 COMPATION: COMPATION: COMPATION: MABER: US/08 Filed Herewis Filed Here	4 S Vati
04470000744806884444		uence 4, Application Uneration Control (1982) APPLICANT: Hillman, Uneration Interaction Interaction: SapelicaNT: Hillman, Uneration: Interaction: SapelicaNT: Hillman, Uneration: Interaction: SapelicaNT: Hillman, Uneration: Interaction: Street: 13174 Porter CITY: Palo Alto STREET: 3174 Porter CITY: Palo Alto STREET: 3174 Porter CITY: Palo Alto STREET: 1374 Porter CITY: Palo Alto STREET: 1374 Porter CITY: Palo Alto COMPUTER: CA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: HIM COMPA CONFUTER: Filed Interaction NUMBER: Filed Interaction NUMBER: Filed Interaction NUMBER: Filed APPLICATION NUMBER: FILING DATE: FILED AND APPLICATION NUMBER: REFERENCE/DOCKET NUM TELECOMMUNICATION NUMBER: REFERENCE/DOCKET NUM TELECANTION FOR SEQ ID NUSBURGES: SINGIA STOPPOLOGY: LINGAT INMEDIATE SOURCE: LIBRARY: GenBank CLONE: 234746	h Similarity 52. 99; Conservative
44466666666666666666666666666666666666		T 1 -8.4-873-4 uence 4, Applicat. uence 4, Applicat. uent No. 58437170 APPLICANT: Hillm APPLICANT: Guegl TITLE OF INVENTION NUMBER OF SEQUENC CORRESPONDENCE ADD ADDRESSE: 1nc; STREET: 3174 P. CITY: Palo Alt. STATE: CA COUNTRY: USA COUNTRY COUNTRY: USA COUNTRY COUNTRY: USA COUNTRY	mila Co
23 86 86 87 84 84 84 84 84 84 84 84 85 86 86 86 86 86 86 86 86 86 86		JET 1 JET 1 JET 1 JET 1 APPLICANT: COMMUTER: OPERATING DAT APPLICATIO FILING DAT APPLICANT: APP	ch 1 Si 99;
4 4 4 4 4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6		1-824-873-4 Ivence 4, p Ivence 4, p Ivence 4, p Ivence 4, p Ivence 1, p Ivence 2, p Ivence 2, p Ivence 2, p Ivence 3, p Ivence 4, p Ivence	Mat Loca es
00000000000000000000000000000000000000		RESULT 1 US-08-824-873-4 Sequence 4, Application US/0882487 Sequence 4, Application US/0882487 GENERAL INFORMATION: APPLICANT: Hillman, Jennifer LAPPLICANT: Gedgler, Karl TITLE OF INVENTION: NOVEL RAB NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: ADDRESSEE: Incyte Paraceut STREET: 3174 Porter Drive CITY: Palo Alto STRATE: GA COUNTRY: USA ZIP: 94304 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DS SOFTWARE: FastSEQ for Window CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/82 FILING DATE: Filed Herewith CLASSIFICATION DATA: APPLICATION NUMBER: PF TILING DATE: A15-85-0555 FILING BATE: A15-85-0555 TELEFHONE: 415-85-0555 TELEFHONE: 415-85-0555 TELEFROMUNICATION INFORMATION: NAME: Billings, Lucy J. REGISTRATION NUMBER: PF TELEFORMUNICATION INFORMATION: NAME: Billings, Lucy J. REGISTRATION NUMBER: PF TELEFORMUNICATION INFORMATION: NAME: Billings, Lucy J. REGISTRATION NUMBER: PF TELEFORMUNICATION INFORMATION: NAME: Billings, Lucy J. REGISTRATION NUMBER: PF TELEFORMUNICATION INFORMATION: NAME: Billings, Lucy J. REGISTRATION NUMBER: PF TELEFORMUNICATION INFORMATION: NAME: Billings, Lucy J. REGISTRATION NUMBER: PF TELEFORMUNICATION INFORMATION: NAME: Billings, Lucy J. REGISTRATION NUMBER: PF TELEFORMUNICATION INFORMATION: NAME: Billings, Lucy J. REGISTRATION NUMBER: PF TELEFORMUNICATION INFORMATION: NAME: BILLING ACCOUNT NUMBER: PF TE	Query Match Best Local S Matches 99
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Sequence 25, Application US/08531525
Patent No. 5840683
GENERAL INFORMATION:
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NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 37-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                      181 RMRASNE 187
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Best Local Similarity
Matches 97; Conservat
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                                                                                                                                                                                                                                 US-08-531-525-25
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                                                                                               61 IWDTAGQERERTITTAYYRGAMGIMLVYDITUEKSFDNIRNWIRNIEEHASADVEKMILG 120
                                                                                                                                                121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                     MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
                     61 IWDTAGGERYQTITKQYYRRAQGIFLYYDISSERSYQHIMKAVSDVDEYAPEGVQKILLG 120
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49.3%; Score 545; DB 3;
Best Local Similarity 52.9%; Pred. No. 3e-52;
Matches 99; Conservative 45; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESG for Windows Version 2.0
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/198,184
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEGUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
STREET: Palo Alto
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
PRIOR APPLICATION:
PRIOR APPLICATION UDATA:
APPLICATION WUMBER: 08/824,873
FILING DATE:
ATTONNEY, AGENT INPORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0240 US
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            NOVEL RAB PROTEIN
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Patent No. 6010859
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl
TITLE OF INVENTION: NOVEL RAB PR
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INFORMATION FOR SED ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 207 amino acids
TYPE: amino acid
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CLONE: 234746
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121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
61 IWDTAGQERFRTITTAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEEHASADVEKMILG 120
                                                                                    62 DTAGQERFRIITTAYY-RAMGIMLUYDITNEKSFDNIRNWIRNIEEHASADVEKMILGNK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hlavka, Joseph J.
APPLICANT: Pincus, Matthew R.
APPLICANT: Pincus, Matthew R.
APPLICANT: Abajian, Henry B.
APPLICANT: Kende, Andrew S.
APPLICANT: Kende, Andrew S.
APPLICANT: TITLE OF INVENTION: Peptides Inhibiting the Oncogenic Action NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 205;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,525
FILING DATE: 21-SEP-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Greenlee and Winner, P.C. 5370 Manhattan Circle, Suite 201
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

December 25, 2004, 01:55:59; Search time 92 Seconds (without alignments) 1325.863 Million cell updates/sec Run on:

US-09-817-198C-2 1105 1 MAKQYDVLFRLLLIGDSGVG......LEEEEGKFEGPANSSKTCWC 212 Title: Perfect score: Sequence:

Scoring table:

1825181 segs, 575374646 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score Watch Length DB ID 1105 100.0 212 1 RB15 HUWAN 1090 98.6 212 1 RB15 HUWAN 1090 97.5 212 1 RB15 FATT 1077 97.5 212 2 Q6D136 1077 97.5 212 2 Q6D136 1086 62.1 143 2 AAH63736 1086 62.1 143 2 AAH63736 1086 62.1 143 2 AAH63736 1087 55.4 210 2 Q9TY82 108 55.7 50.4 211 2 Q9TY82 108 55.7 50.4 211 2 Q9TY82 108 545.5 49.3 207 1 RB8A CANPA 1080 207 2 Q8VCF6 1080 207 2 Q8VCF6 1080 207 2 Q8VCF6 1080 207 2 Q6DQV5	-		عد ا			SUMMARIES	
1105 100.0 212 1 RB15 HUMAN PS9190 homo see	CQ:	Score	Query	Length	BB	i	
1090 98.6 212 1 RB15_MOUSE 2086286 mus mus mus		1105	100.0	212	-	RB15 HUMAN	homod
1077 97.5 212 1 RB15_RAT Q66136 brachvos 686 62.1 143 2 Q61736 Q6412 Acnopus 686 62.1 143 2 Q61736 Q6412 Acnopus 686 62.1 143 2 Q61736 Q6412 Acnopus 686 62.1 143 2 Q61742 Acnopus 686 62.1 143 2 Q61742 Acnopus 686 62.1 143 2 AAH6736 Acnopus Acnopus 686 62.1 143 2 AAH6736 Acnopus Acnopus 686 62.1 143 2 AAH6736 Acnopus Acnopus 686 62.1 143 2 Q61742 Acnopus 686 62.1 143 2 AAH6736 Acnopus 686 62.1 143 2 AAH6736 Acnopus 691 691 691 691 691 691 691 691 691 691	1 (1	1090	98.6	212	Н	RB15_MOUSE	
872 78.9 212 2 Q6D136 Q664136 D664136 brachyc 6 66 62.1 143 2 Q6P442 Q6P442 Q6P4790 mus	· C	1077	97.5	212	Н	RB15_RAT	
798 72.2 168 2 Q91YWO C91YWO MUS mus mus <t< td=""><td>4</td><td>872</td><td>78.9</td><td>212</td><td>~</td><td>Q6D1<u>3</u>6</td><td></td></t<>	4	872	78.9	212	~	Q6D1 <u>3</u> 6	
686 62.1 143 2 QGP412 QGP412 AAH63736 AAH63737 AAH63736 AAH63737 AAH63736 AAH63737 AAH63736 AAH63736 AAH63736 AAH63736 AAH63736 AAH63736 AAH63737 AAH63736 AAH63736 AAH63736 AAH63736 AAH63736 AAH63736 AAH637376 AAH6	ß	798		168	7	Q91YW0	
686 62.1 143 2 AAH63736 AAH637376 AAH637376 AAH637376 AAH637376 AAH637376 AAH637377 AAH637377 AAH637377 AAH637377 AAH637377 AAH637377 AAH637377 AAH637377 AAH637377 AAH63777 AAH63777 AAH63777 AAH63777 AAH63777 AA	و ا	989	62.1	143	7	Q6P412	
563.5 51.0 200 2 Q7T3A4 Q7C3A4 Drachy 557 50.4 211 2 Q9TYS2 Generol 557 50.4 211 2 Q9TYS2 Generol 545.5 49.5 204 2 O15971 Grosopl 545 49.3 207 1 RBBA_CANFA P61006 Ganis 545 49.3 207 1 RBBA_THUMAN P61006 Ganis 5 54 49.3 207 2 ARP55848 P61006 Ganis 5 53 49.1 207 2 ARP56848 Dromo 8 5 538.5 48.7 201 2 GBOCFG Q644y5 Dromo 5 538.5 48.7 201 2 GBOCFG Q644y5 Drachy 5 538.5 48.7 201 2 GBOCFG Q644y5 Drachy 5 538.5 48.4 200 2 GAFW9 Q644y5 Drachy 5 538.5 48.4 200 2 GAFW9 Q644y5 Drachy 5 538.5 48.4	7	989	62.1	143	0	'n	Aah63736 xenopus l
557 50.4 211 2 Q9TYS2 Q9FYS2 caenority 565 50.4 211 2 MADOTO34 Baddy034 caenority 545 49.3 207 1 RB8A_CANFA P61007 canis 545 49.3 207 1 RB8A_CANFA P61007 canis 545 49.3 207 1 RB8A_CANFA P61007 canis 541 49.0 207 2 Q8VCF6 P61006 home st 559.5 48.8 210 1 RABB_DISOM P6200F6 m cell 536 48.8 200 2 Q6DWLD Q64QY5 Dacabys 534.5 48.4 200 2 Q6DWLD Q64QY5 Dacabys 531.5 48.1 201	ω	563.5	51.0	200	7	Q7T3A4	Q7t3a4 brachydanio
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541 49.0 207 2 QBVCF6 QBVCF6 QBVCF6 m cell 5539.5 48.8 210 1 RABB_DISOM P22128 discopy 558.5 48.8 210 1 RABB_DISOM Q6dQY5 Q6dQY5 558.4 58.4 206 2 Q6DW12 Q6dQY5 Q6dQY5 D8cachyv 534.5 48.4 200 2 Q6PAM9 Q6dqY5 D8cachyv D8cachyv 534.5 48.4 200 2 Q6PAM9 Q6dqY5 D8cachyv D8cachyv 532.4 48.4 200 2 Q6PAM9 Ach60015	14	545	9	207		AAP35848	3 homo
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7 538.5 48.7 201 2 06D0V5 Q6dgy5 brack 3 534.5 48.8 206 2 Q6DXL2 Q6dkl2 brack 5 534.5 48.4 200 2 AAH60015 Q6GWL2 xept 5 53.4 8.4 200 2 AAH60015 AAH60015 xept 5 53.2 48.1 2.0 2 AAH60015 P5115 homo 5 53.4 48.1 2.0 1 RB13 HUMAN Q6GPG6 homo 5 53.5 48.0 2.0 1 RB10 DISOM P52127 disc 5 530.5 48.0 2.0 1 RB10 CANPRA P61026 homo 5 530.5 48.0 2.0 1 RB10 MOUSE C640356 homo 5 530.5 48.0 2.0 1 RB10 MOUSE C640358 homo 5 530.5 48.0 2.0 1 RB13 RAT P51228 ratt 7 530.5 47.8 2.0 1 RBBB MOUSE P61028 mus 8 528.5 47.8 2.0 1 RBBB MOUSE P61028 mus 8 528.5 47.8 2.0 1 RBBB MOUSE P70550 ratt	16		8	210		RAB8_DISOM	
316 48.5 206 2 Q6DKL2 Q6GKL2 ratti 954.5 48.4 200 2 Q6PAW9 Q6GKL2 ratti 154.5 48.4 200 2 Q4H6015 Aah60015 Aah60015 1 203 1 RB13 HUMAN Q6GPG P51153 homo 2 48.1 203 1 RB10 DIGG P51153 homo 3 531.5 48.1 200 1 RB10 DIGG P24409 530.5 48.0 200 1 RB10 LCANFA P6409 P6409 530.5 48.0 200 1 RB10 HUMAN P64027 mus P6407 530.5 48.0 200 1 RB10 HUMAN P64027 mus P64027 mus 530.5 48.0 200 1 RB13 RAT Q9233584 ho P64027 mus 528.5 47.8 207 1 RBBB MOUSE P64028 mus P64028 mus 528.5 47.8 207 1 RBBB MOUSE P70550 ratt	17	538.5	ω	201		Q6DGVS	
534.5 48.4 200 2 Q6PAM9 Q6PAM9 Q6PAM9 Q6PAM9 Q6PAM9 Q6PAM9 Q6PAM9 AAM6015 xeno 534.5 48.4 200 2 AAH6015 F811.5 P51153 DAM6015 xeno 532 48.1 218 2 Q6GPG6 P51153 DAM0 Q6GPG6 P51153 DAM0 530.5 48.0 200 1 RB10_LDKSM P61026 P61026 DAM0 530.5 48.0 200 1 RB10_LWAN P61026 DAM0 530.5 48.0 200 1 RB13_RAT Q693364 DR3584 DR3584 DR3584 DR3584 DR3584 DR3586 DAM0 P61027 MAW P61027 MAW P61028 DAM0 P61028	18	536	8	206		Q6DKL2	
534.5 48.4 200 2 AAH60015 AAB60015 xell 1 532 48.1 2.03 1 RB13 HUMAN Q65PG6 3 23.1 48.1 2.03 1 RB10 DISOM Q65PG6 homo 3 531.5 48.1 2.00 1 RB10 CANFA P241273 Homo 4 530.5 48.0 2.00 1 RB10 CANFA P61026 homo 5 530.5 48.0 2.00 1 RB10 MOUSE P61026 homo 6 530.5 48.0 2.00 1 RB10 MOUSE Cq63784 P61026 homo 7 530.5 48.0 2.00 1 RB10 MOUSE Cq63784 P61027 mus 8 528.5 47.8 2.07 1 RBBB HUMAN P61028 mus P61028 mus 9 528.5 47.8 2.07 1 RBBB MOUSE P61028 mus 1 528.5 47.8 2.07 1 RBBB RDAT P70550 ratt	19	534.5	8	200		Q6PAW9	Ocpaw9 xenopus lae
532 48.1 203 1 RB13 HUMAN P51153 homo 532 48.1 218 2 GGGPG QGGPG QGGPG QGGPG P22127 disponsa 351.5 48.0 200 1 RB10 DISOM P22127 disponsa P24409 cani P24409 cani P6126 homo P6126 homo P6127 disponsa P6126 homo P6102 homo	20	534.5	8	200		AAH60015	Aah60015 xenopus l
2 532 48.1 218 2 QGGPG6 QGGPG6 QGGPG6 homo 3 531.5 48.1 200 1 RB10_DISOM P24127 disc. 5 30.5 48.0 200 1 RB10_HUMAN P24102 canis 6 530.5 48.0 200 1 RB10_HUMAN P61026 homo 7 530.5 48.0 200 1 RB13_RAT Cad33584 Cad33584 8 203 1 RB13_RAT Q92230 homo P51228 ratu 9 528.5 47.8 207 1 RB8B_MOUSE P61028 mus 1 RB8B_MOUSE P61028 mus P61028 mus 9 528.5 47.8 207 1 RB8B_MOUSE P70550 ratt	21	532	œ	203		RB13 HUMAN	homo
3 531.5 48.1 200 1 RB10_CANFA P24409 canis 4 530.5 48.0 200 1 RB10_CANFA P24409 canis 5 530.5 48.0 200 1 RB10_HUMAN P61026 homo 6 530.5 48.0 200 1 RB10_HUMAN P61026 homo 7 530.5 48.0 200 2 CAG33584 P61027 mus 8 528.5 47.8 207 1 RB13_RAT P35286 ratt 9 528.5 47.8 207 1 RB8B_HUMAN P61028 mus 9 528.5 47.8 207 1 RB8B_RATE P70550 ratt 1 528.5 47.8 207 1 RB8B_RATE P70550 ratt	22	532	œ	218		<u> Д</u> 6G <u>Р</u> G6	homo
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5 530.5 48.0 200 1 RBIO_HUMAN P61026 homo 6 530.5 48.0 200 1 RBIO_MOUSE Cad33584 homo 7 530.5 48.0 200 2 CAG33584 Cad33584 homo 8 528.5 47.8 203 1 RB13_RAT P53286 ratt 9 528.5 47.8 207 1 RB8B_HUMAN Q92930 homo 9 528.5 47.8 207 1 RB8B_MOUSE P61028 mus 1 528.5 47.8 207 1 RB8B_RAT P70550 ratt	24	$\overline{}$	ω,				
6 530.5 48.0 200 1 RB10_MOUSE P64.027 mus 7 530.5 48.0 200 2 CAG33584 CAG33584 ho 8 528.5 47.8 203 1 RB13_RAT P55286 ratt 9 528.5 47.8 207 1 RB8B_HUMAN P61028 mus 5.28.5 47.8 207 1 RB8B_MOUSE P61028 mus 1 528.5 47.8 207 1 RB8B_RAT P70550 ratt	25	\sim	ω.			RB10 HUMAN	
7 530.5 48.0 200 2 CAG33584 Cag33584 ho 8 528.5 47.8 203 1 RB13 RAT P35286 ratt 9 528.5 47.8 207 1 RB8B HUMAN Q09393 homo 528.5 47.8 207 1 RB8B MOUSE P61028 mus 1 528.5 47.8 207 1 RB8B MOUSE P70550 ratt	26	\sim	8			RB10 MOUSE	P61027 mus musculu
8 528.5 47.8 203 1 RB13 RAT P35286 ratt 9 528.5 47.8 207 1 RB8B HUMAN Q292930 homo 0 528.5 47.8 207 1 RB8B MOUSE P61028 mus 1 528.5 47.8 207 1 RB8B_RAT P70550 ratt	27	$^{\circ}$	8			CAG33584	Pomod 4
9 528.5 47.8 207 1 RB8B_HUMAN Q92330 homo 528.5 47.8 207 1 RB8B_MOUSE P61028 mus 1 528.5 47.8 207 1 RB8B_RAT P70550 ratt	28	m	7.				att
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1 528.5 47.8 207 1 RB8B_RAT P70550 rattus	30	m	7.			RB8B_MOUSE	mus mu
	31	m				RB8B_RAT	70550 rattus

32 528.5 47.8 207 2 018336 34 526 47.6 202 1 RB13 MOUSE 35 526 47.6 202 1 RB13 MOUSE 36 523.5 47.4 204 2 070261 37 521 47.1 206 2 09HET4 38 520.5 47.1 206 2 09HET4 39 520.5 47.1 206 2 09TB2 40 518 46.9 205 2 0770B2 41 518 46.9 215 2 077497 42 515 46.6 216 2 06L502 44 515 46.6 216 2 06L502	O18338 drosophila	ייניים יייי פניינים	Opdd03 mus musculu	P55258 mus musculu	Q7qeg1 anopheles g				Q7rvg3 neurospora					Q9fjfl arabidopsis
528.5 528.5 528.5 526.47.6 523.5 521.47.1 520.5 47.1 518.46.9 518.46.9 518.46.9 515.5 515.5 515.5	018338	BAD0 / 0.38	RB13 MOUSE	RB8A MOUSE	Q7QEG1	Q9HET4	Q7PUB2	024466	Q7RVG3	040218	Q7XHP7	040215	Q6L502	Q9FJF1
528.5 528.5 526.47.8 526.47.6 523.5 521.47.1 520.5 47.1 520.5 47.1 518.46.9 518.46.9 515.5 46.7 515.5 46.7	010	7	-	7	0	0	~	7	8	7	7	7	~	7
528.5 528.5 526.5 526.5 521.5 518 518 518 518 515 515	207	707	202	206	204	206	299	216	205	214	215	216	216	216
	47.8	47.8	47.6	47.6	47.4	47.1	47.1	47.0	46.9	46.9	46.9	46.7	46.6	46.6
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	32	33	34	35	36	37	38	6.6	40	41	42	43	44	45

# ALIGNMENTS

HUMAN STANDARD; PRT; 212 AA.  RBB15 HUMAN STANDARD; PRT; 212 AA.  28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 44, Last sequence update) 25-FEB-2003 (Rel. 44, Last annotation update) 05-JUL.2004 (Rel. 44, Last annotation update) Ras-related protein Rab-15.  Name=RABLS; Homo sapiens (Human).  BUARTYOCA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBI_TAXID=9606;	SEQUENCE FROM N.A.  MEDILINE-2245983; PubMed=12508121; DOI=10.1038/nature01348;  Heilig R., Eckenberg R., Petit JL., Fonknechten N., Da Silva C.  Catcolico L., Levy M., Barbe V., De Berardinis V., Ureta-vidal A.,  Palletier E., Vico V., Anthouard V., Rowen L., Madan A., Oin S.,  Sun H., Du H., Pepin K., Artiguenave F., Robert C., Cruaud C.,  Sun H., Du H., Pepin K., Artiguenave F., Robert C., Cruaud C.,  Cure S., Segurens B., Aniere F., Samson G., Brottier P.,  Aiach N., Boscus D., Dickhoff R., Dors M., Dubois I., Friedman C.,  Gouyvenoux M., James R., Madan A., Mairey-Bertrada B., Mangenot S.,  Martins N., Menard M., Oztas S., Ratcliffe A., Shaffer T., Trask B.,  Vacherie B., Bellemere C., Belser C., Besnard-Gonnet M.,  Dufosse-Laurent V., Ferron C., Lechaplais C., Louesse C.,  Magdelent G., Patent B., Petit E., Sirvain-Trukniewicz P., Trybou A.,  Weg-Czarny N., Bataille B., Bluet B., Bordelais I., Dubois M.,  Dumont C., Guerin T., Haffray S., Hammadi R., Muanga J., Pellouin V.,  Robert D., Wunderle B., Gauguet G., Roy A., Sainte-Marthe L.,  Verdier J., Verdier-Discala C., Hillier L.W., Fulton L., McPherson J.,  Quetier F., Waterston R., Hood L., Weissenbach J.;  "The DNA sequence and analysis of human chromosome 14.";  Nature 421:601-607(2003).	TISSUEBRAIN,  TISSUEBRAIN,  THEOLINE-22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;  MEDLINE-22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;  Strauthers R.L., Feingold E.A., Grouse L.H., Derge J.G.,  Klauuner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  Altschul S.F., Joedan H., Moore T., Max S.I., Wang J., Hsieh F.,  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  Stapleton M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.B.,  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  Raha S.S., Loquellano N.A., Peters G.J., Abramon R.D., Mullahy S.J.,  Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  Villalon D.K., Madan A., Rodrigues S., Sanchez A.,  Whithing M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
RESULT 1 RB15 HUMAN LD RB15 HUMAN AC P59150; 0861 DT 28-FEB-2003 DT 28-FEB-2003 DT 05-UUL-2004 DE RAB-related GN Name-RAB15; OS HOMO Sapien CO BUKARYOTA; N CO MAmmalia; B; CO NCBI_TAXID=3	SEQUENCE F WEDLINE-22 Hellin R-22 Cattolico Cattolico Sun H., Du Bruels T., Gouyvenoux Martins N., Gouyvenoux Martins N., Vadherie B Bartol-Max Dufonse-La Magdelenal Wega-Czarr Dumont C., Verdier J. Verdier J. Watsuda F.	SEQUENCE E TISSUB-BYZ MEDLINDE-ZZ Strausherz Altschul & Altschul & Staplechenk Staplechenk Staplechenk Brownstein Brownstein Brownstein Raha S.S., Raha S.S., Raha S.S., Rulalan I
RESULT ID RI ID AC DT 22 PP DT 22 PP CO DE RO CO	8	R B B B B B B B B B B B B B B B B B B B

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8

121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNINIKESFTRLTELVLQAHRKELEGI

61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120

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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marza M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-geranylgeranyl cysteine (By
similarity).
YapmolyKillgebokRQVGREQGQQLAKEYGMPFYE
TSACTNINIKESFTRLTELVLQAHRKELEGIRMRANBLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AELEEEEGKPEGPANSSKTCWC -> VGDATGLPGCGEGAS
PGKARRGPDGKANARKLCLPQPWMKTSGTHQKASRRSLLG
IRLMRSRNGBWEBSKGSSWRRSMANTSMKQVPAPTSTLKSH
SRV (in 1seform 2).
/FIId=VSP 010420.
D16A0C71797ED782 CRC64;
                                                                                                                                                         TISSUE=Flacenta;
Li W. B., Gruber C., Jessee J., Polayes D.;
Li W. B., Gruber C., Jessee J., Polayes D.;
"Full-length cDNA libraries and normalization.";
Submitted (FEB-2003) to the EMBJ/Genbank/DDBJ databases.
--- FUNCTION: May act in concert with RAB3A in regulating aspects of synaptic vesicle membrane flow within the nerve terminal (By
                                                                                                                                                                                                                                                                                                                                                                                      Note=No experimental confirmation available;
SIMILARITY: Belongs to the small GTPase superfamily. Rab family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P32939; IKY3.

Genew; HGNC.20150; RAB15.

InterPro; IPR003579; GTP8ae Rab.

InterPro; IPR001606; Ras tringfrung.

InterPro; IPR005225; Small GTP.

Pfam; PR00011; Ras; 1.

PRINTS; PR000149; RASTRNSFRMG.

SMART; SM00175; RaB; 1.

TIGRFAMs; TIGR00231; small GTP; 1.

Alternative splicing; GTP-Einding; Lipoprotein; Prenylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTP (By similarity).
GTP (By similarity).
GTP (By similarity).
S-geranylgeranyl cysteine (By similarity).
                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                        Name=2;
IsoId=P59190-2; Sequence=VSP_010420;
                                                                                                                                          SEQUENCE OF 42-212 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                       IsoId=P59190-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL139022; -; NOT ANNOTATED_CDS.
EMBL; BC040679; AAH40679.2; -.
EMBL; BX248046; CAD62353.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 AA; 24390 MW;
                                                                                                                                                                                                                                                                          similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
67
124
210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein transport. NP BIND 15 NP BIND 63 NP BIND 121 1 LIPID 11P 121 1 LIPID 210 2
                                                                                                                                                                                                                                                               similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212
                                                                                                                                                                                                                                                                                                                          Name=1;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI_TaxID=10090,

Mus musculus (Mouse)

Name=Rab15;

SEQUENCE FROM N.A.

28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 20-UUL-2004 (Rel. 44, Last annotation update) Ras-related protein Rab-15.

212 AA

RB15 MOUSE Q8K386;

RB15_MOUSE

REAL MEDILINE-1238857; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Sthaefer C.F., Bhar N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Stapleton M.J., Usdin T.B., Parmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaraten P.H.,
RA Boask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaraten P.H.,
RA Rohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Raha S.C., Carimwood J., Schevchenko Y., Bouffard G.G.,
Mitting M., Madan A., Youchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Generation and initial analysis of more than 15,000 full-length human mouse conna equal concert with RAB3A in regulating aspects of
Symptic vesicle membrane flow within the nerve terminal (By This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifised and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-eib.ch). similarity). SMART; SM0175; RAB; 1.
TIGREAMS; TIGR00231; small_GTP; 1.
GTP-binding; Lipoprotein; Prenylation; Protein transport.
NP_BIND 15 22 GTP (By similarity). HSSP; P32939; 1KY3. MGD; MGI:1916865; Rab15. GO; GO:0005515; F:protein binding; IPI. InterPro; IPR003879; GTPase Rab. InterPro; IPR001806; Ras trinsfrung. InterPro; IPR005225; Small_GTP. EMBL; BC027769; AAH27769.1; -. PRINTS; PR00449; RASTRNSFRMNG. Pfam; PF00071; Ras; 1 

61 IMDIAGGERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQXILIG 120

100.0%; Score 1105; DB 1; Length 212; 100.0%; Pred. No. 7.9e-79; .ive 0; Mismatches 0; Indels 0

212; Conservative

Matches

g ò

Query Match Best Local Similarity

Gaps

; 0

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5.1.6
Compugen Ltd.
 GenCore version (c) 1993 - 2004
           Copyright
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OM protein - protein search, using sw model

December 25, 2004, 05:09:38 ; Search time 78 Seconds (Without alignments) 261.512 Million cell updates/sec Run on:

US-09-817-198C-2

1105 1 MAKQYDVLFRLLLIGDSGVG......LEEEEGKPEGPANSSKTCWC score: Title: Perfect so Sequence:

212

283416 segs, 96216763 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 4 2 6 4 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description		-	Д						GTP-binding protei		GTPase AtRAB8 - Ar	hypothetical prote	Ω											Sec4p homolog - ye	rot		pinding		
	OI	F42148	T33855	B49647	B36364	A49647	A38625	D36364	B38625	178851	B42148	T45901	T28971	833900	T48378	812790	T14565	S57478	JS0640	T14405	S57471	836365	S57462	S51495	JC7589	S57474	A34716	A38202		S38740
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	Match Length		224	207	207	203	200	200	209	206	200	216	201	216	216	200	215	215	216	222	216	217	215	203	204	215	208	208	203	202
ئ ئ	Match	7.5	50.6	49.3	49.3	48.1	48.1	48.0	48.0	47.6		•	•	46.3	•	46.2		46.0	46.0	45.9		٠	45.5	45.3	44.8	•		43.7	43.6	43.4
	Score	107	559	545	545	~	531.5		530	526	522.5	519	514	512	512	510	509	508.5	208	507.5	206	505.5	502.5	501	495.5	492.5	483.5	483	482	480
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GTP-binding protei	ARA-5 [imported] -	GTP-binding protei	GTP-binding protei	hypothetical prote	GTP-binding protei	ras protein homolo	GTP-binding protei	GTP-binding protei	GTP-binding protei	GTP-binding protei					
B34716	872515	JC2488	JC4105	JC5337	841430	B86153	JC1247	830096	T33781	T14391	T18242	B38202	TVBYQ4	538339	TVRTYP
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203	202	201	203	201	202	258	203	203	205	206	210	203	215	205	205
43.3 203		- •				•	•		••	•			•		•
	43.3	43.2	43.2	43.2	43.2	43.1	43.0	43.0	42.9	42.8	42.8	42.6	42.6	42.4	42.4

# ALIGNMENTS

		40.2
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ESULT	42148	TO-hir

F42148
GTP-binding protein rabl5 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-56P-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: F42148
R;Elferink, L.A.; Anzai, K.; Scheller, R.H.
J. Biol. Cham. 267, 5768-5775, 1992
A;Title: rabl5, a novel low molecular weight GTP-binding protein specifically expressed 1
A;Reference number: A42148
A;Status: preliminary
A;Molecule type: mRNA
A;Status: preliminary
A;Molecule type: mRNA
A;Status: preliminary
A;Molecule type: mRNA
C;Status: preliminary
C;Keywords: 1-212 < ELF>
A;Cross-references: UNIPROT:P35289; GB:M83679; NID:g206536; PIDN:AAA41995.1; PID:g206537
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
C;Keywords: GTP binding; lipoprotein; nucleotide binding; P-loop; prenylated cysteine
F;9-124/Region: nucleotide-binding motif A (P-loop)
F;12-124/Region: GTP-binding NKXD motif F;120,212/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted

.; 0 Query Match

97.5%; Score 1077; DB 2; Length 212;
Best Local Similarity 97.6%; Pred. No. 1e-78;
Matches 207; Conservative 2; Mismatches 3; Indels

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9 1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ à

9 1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ g 61 IMDTAGQERYQTITKQYYRRAQGIFLUYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120 ò

NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180 121 셤 δ

g

RMRASNELALAELEEEGKPEGPANSSKTCWC 212 181 à 셤

181

RESULT 2

733855
hypothetical protein D1037.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Sate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-Jan-2000
C;Accession: T33855
R;Ledwith, J.; Blewald, T.
R;Ledwith, J.; Blewald, T.
R;Despecies: R;Best Data Library, November 1998
A;bescription: The sequence of C. elegans cosmid D1037.

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Local Similarity 52.9
nes 99; Conservative
                                                                                                                                                                                                                                                                                                      181 RMRASNE 187
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849647

GTP-binding protein rab8 - human

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C;Accession: B49647; S36817

B;Zahraouli, A.; Joberty, G.; Arpin, M.; Fontaine, J.J.; Hellio, R.; Tavitian, A.; Louvar, J. Cell Biol. 124, 101-115, 1994

A;Title: A small rab GTPase is distributed in cytoplasmic vesicles in non polarized cell A;Reference number: A49647; MUID:94124602; PMID:8294494

A;Accession: B49647

A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL:X56741; NID:g452317; PIDN:CAA40065.1; PID:g4523
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A:Reference number: 836817; MUID:93387463; PMID:8375503

A:Accession: 836817

A
                                                                                                                                                                                                                                                               %)Gene: CESP:D1037.4
A;Map position: 1
A;Introns: 10/3; 62/2; 82/3; 181/1
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
A;Reference number: 221424
A;Accession: T33855
A;Accession: T33855
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-224 <LED>A;Cross-references: EMBL.AF106592; PIDN:AAC78494.1; GSPDB:GN00019; CESP:D1037.4
A;Experimental source: strain Bristol N2; clone D1037
A;Genetics:
A;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIEVDGIKVRIQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 50.6%; Score 559; DB 2; Length 22 Best Local Similarity 55.3%; Pred. No. 2.2e-37; Matches 105; Conservative 42; Mismatches 39; Indels
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A; Residues: 1-207 <ZAH>
A; Cross-references: UNIPROT:P61006; EMBL::
R; Joberty, G.; Tavitian, A.; Zahraoui, A.
FEBS Lett. 330, 323-328, 1993
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177 EMRAATGAAI 186
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A;Accession: B36364
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-207 < CHA>
A;Residues: 1-207 < CHA>
A;Residues: 1-207 < CHA>
A;Residues: 1-207 < CHA>
A;Cross-references: UNIPROT:P61007; GB:X56385; NID:g920; PIDN:CAB56776.1; PID:g6006436
C;Superfamily: ras transforming protein; membrane trafficking; nucleotide binding; P-loop; E; P:124,Domain: translation elongation factor Tu homology < FTU>
F;12-124/Region: GTP-binding motif A (P-loop)
F;15-123/Region: GTP-binding SAK/L motif
F;151-153/Region: GTP-binding SAK/L motif
F;151-153/Region: GTP-binding SAK/L motif
F;204/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
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C;Species: Homo sapiens (man)
C;Species: 33-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A9547
R;Zahraoui, A.; Joberty, G.; Arpin, M.; Fontaine, J.J.; Hellio, R.; Tavitian, A.; Louvard
J. Cell Biol. 124, 101-115, 1994
A;Title: A small rab GTPase is distributed in cytoplasmic vesicles in non polarized cells:
A;Reference number: A49647; MUID:94124602; PMID:8294494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTP-binding protein rab8 - dog
Cispecies: Canis lupus familiaris (dog)
Cibate: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
Cibaccesion: B36364; S15604
Richavrier, P.; Vingron, M.; Sander, C.; Simons, K.; Zerial, M.
Mol. Cell. Biol. 10, 6578-6585, 1990
A;Title: Molecular choning of YPTI/SBC4-related cDNAs from an epithelial cell line.
                                                                                                                                                         180
                                          61 IMDTAGGERFRITTTAYYRGAMGIMLVYDITNEKSFDNIRNWIRNIEBHASADVEKMILG 120
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IWDTAGQERYQTITKOYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
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52.9%; Pred. No. 2.6e-36;
cive 45; Mismatches 43; Indels
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A,Molecule type: mRNA
A,Residues: 1-203 <ZAH>
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

December 25, Run on:

2004, 01:51:44 ; Search time 308 Seconds (without alignments) 246.918 Million cell updates/sec

US-09-817-198C-2 score: Perfect

1105 1 MAKQYDVLFRLLLIGDSGVG......LEEEEGKPEGPANSSKTCWC

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2001as:* geneseqp2003as:* A Geneseq 23Sep04:* ......... Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

# Rea

Description	Abp62882 Human pol		Aaul7136 Novel sig	Adb93844 Human nov	Aab41604 Human ORF	м	Aaul7555 Novel sig	Human	e	Abb70670 Drosophil	Ade58121 Human Pro	Abb11916 Human rab	Abp41333 Human ova	Ade83429 Human Pro	Ade58125 Human Pro	Aab58196 Lung canc	Aab09979 Human Rab	Aab19165 Amino aci	Aab95340 Human pro	2 Antips		99		Aag67154 Amino aci	Aab92628 Human pro
ΩI	ABP62882	AAE29096	AAU17136	ADB93844	AAB41604	ADE58127	AAU17555	ADB94263	ADJ71123	ABB70670	ADE58121	ABB11916	ABP41333	ADE83429	ADE58125	AAB58196	AAB09979	AAB19165	AAB95340	ADN05082	AAB56993	ABG07266	ABB71647	AAG67154	AAB92628
DB	្រែ	ဖ	4	7	m	7	4	7	7	4	7	4	വ	7	7	ო	m	m	4	80	m	4	4	4,	4
& Query Match Length	212	212	401	401	218	212	188	188	208	204	207	213	221	203	203	246	200	200	200	200	218	218	207	207	207
Query Match	100.0	100.0	100.0	100.0	98.8	97.5	75.3	75.3	51.9	49.5	49.3	49.3	48.9	48.1	48.1	48.1	48.0	48.0	48.0	48.0	48.0	47.9	•	47.8	47.8
Score	1105	1105	1105	1105	1092	1.077	832	832	~	546.5	545	545	540	532	532	532	530.5	530.5	530.5	530.5	530.5	529.5	528.5		528.5
Bult No.		7	٣	4	ß	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	

Abp65204 Hypoxia-r	Adh68266 Human G-p	Adj69495 Human hea	Aab09982 Canine Ra	Aab09980 Human Rab	Aab09981 Human Rab	Abj26542 Aspergill			Aag08688 Arabidops	Aag53944 Arabidops	Aag08687 Arabidops	Aao19956 C elegans	Aag35215 Zea mays	Aao26373 Ras-like	Adn72851 Thale cre	Aag19220 Arabidops	Aag08006 Arabidops	Abg23365 Novel hum	Aag47826 Arabidops
ABP65204	ADH68266	ADJ69495	AAB09982	AAB09980	AAB09981	ABJ26542	ABJ25583	AAG53945	AAG08688	AAG53944	AAG08687	AA019956	AAG35215	AA026373	ADN72851	AAG19220	AAG08006	ABG23365	AAG47826
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47.8	47.8	47.6	47.6	47.3	47.3	47.3	47.3	47.0	47.0	47.0	47.0	46.5	46.5	46.3	46.3	46.2	45.9	45.8	45.3
528.5	528.5	526.5	526	523	523	523	523	519	519	519	519	514	513.5	512	512	510	507	506.5	501
26	27	58	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Human, vulnerary, dermatological, neuroprotective, nootropic, cancer, antiparkinsonian, immunostimulant, cytostatic; immunosuppressive; antidiabetic; antialiergic; gene therapy, wound healing; tissue repair; burn; central nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy. Ź Human polypeptide SEQ ID NO 319. ABP62882 standard; protein; 212 (first entry) 14-OCT-2002 ABP62882; RESULT 1 ABP62882 

sapiens. Homo

WO200218424-A2.

07-MAR-2002.

31-AUG-2001; 2001WO-US027093.

01-SEP-2000; 2000US-00654935

(HYSE-) HYSEQ INC.

Wang J; Zhang J, Ren F, Zha Wehrman T; Asundi V, Zhou P, Xue AJ, Wang D, Liu C, Drmanac RT, Wang D, Tang YT, Zhao QA,

WPI; 2002-583321/62. N-PSDB; ABQ93361 New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.

Claim 20; SEQ ID NO 319; 284pp + Sequence Listing; English.

The invention relates to an isolated polynucleotide (I) comprising one of 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II). (II) and (III) are useful for diagnostic evaluation of disorders (I) is useful for gene therapy of diseases and (II) can be used for

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therapeutic treatment. Diseases that may be treated include wound healing
                                                                                                                                                                                                                                                                              61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPEGVQKILIG 120
                                                                                                                                                                                                                                                                                                  NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQAHRKELEGL 180
                                                                                                                                                                                                                                                                                                                                                        immunodeficiency; neurodegenerative; Alzheimer's disease; cirrhosis; Parkinson's disease; wasting disease; cachexia; myocardial infarction; osteoporosis; atherosclerosis; glomerulonephritis; Crohn's disease; irriteble bowel syndrome; multiple sclerosis; osteoarthritis; allergy; pancreatitis; autoimmune thyroiditis; rheumatoid arthritis; osteopathic; pancreatitis; asyndrome; infection; transgenic; gene therapy; nootropic; out; neuroprotective; vasotropic; cytostatic; dermatological; nephrotropic; gout; ophthalmological; tranquilliser; cancer; stroke; Grave's disease; AIDS; asthma; anaemia; drug screening.
                                                                                                                                                                                                                                       9
            and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies. Note The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                     1 MAKQYDVLFRLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIRVDGIKVRIQ
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; Ras-like protein; inflammation; cell proliferation; apoptosis;
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                                                                                                                                                                  DB 5; Length 212;
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.94
te= "Protein kinase C phosphorylation site"
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136. .141
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                                                                                                                                                             Score 1105; DB 5;
Pred. No. 2e-108;
; Mismatches 0;
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:e= "N-myristoylation site"
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/note= "N-glycosylation site"
206. .208
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100.0%; Pr
tive 0;
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Best Local Similarity 100.
Matches 212; Conservative
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29. .32
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/note= "
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The invention relates to human Ras-like protein and its corresponding nucleic acid. The Ras-like protein and DNA is useful in the development of human therapeutics and diagnostic compositions. They are useful in the diagnosis, prevention and tagnostic compositions. They are useful in the associated with cell proliferation and apoptosis, e.g. AIDS and other confections or genetic immunodeficiencies, neurodegenerative disease e.g. Rafections or genetic immunodeficiencies, neurodegenerative disease e.g. Alzheimer's disease, Parkinson's disease, wasting diseases e.g. cachexia, is chaemic injuries e.g. myocardial infarction, stroke or reperfusion cinjury, toxin-induced diseases such as alcohol-induced liver damage or cirrhosis, osteoporosis or cancer. They are also used to treat disease, astenment, anaemia, Crohn's disease, diabetes mellitus, contractions, astenment, anaemia, Crohn's disease, diabetes mellitus, contractions, multiple sclerosis, osteoarthritis, pancreatitis, autoimmune thyroiditis, rheumatoid arthritis, Sjogren's syndrome, uveitis, trauma, or viral, bacterial, fungal, parasitic, protozoal or helminthic infections. The antibodies of the invention are useful in pharmacogenomic analysis or for tissue typing. The transgenic animals are constituted by streaming assays and its DNA is used in gene therapy. The present constitution of a Ras-like protein is used in gene therapy. The present
                                                                                                                                                                                                                                                                                                                   New isolated human Ras-like protein polypeptide, useful for diagnosing, treating or preventing inflammation and disorders associated with cell proliferation and apoptosis, e.g. AIDS, cancer, allergies, anemia, asthma
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 /note= "Protein kinase C phosphorylation site"
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iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 74; 82pp; English.
                                                                                                                                                                                                                             Di Francesco V,
                                                                                                              27-MAR-2002; 2002WO-US009328.
                                                                                                                                                  27-MAR-2001; 2001US-00817198
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AAU17136 standard; protein; 401 AA.

Modified-site

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Sequence 1, Appli
Sequence 21, Appli
Sequence 2111, Ap
Sequence 151, Ap
Sequence 1212, Ap
Sequence 1212, Ap
Sequence 18, Appl
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Sequence 28, Appl
Sequence 29, Appl
Sequence 7830, Ap
Sequence 30, Appl
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| cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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| cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
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Compugen Ltd.
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US-09-817-198A-3

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US-10-257-166-152

US-09-764-868-88

US-09-817-198A-28

US-09-817-198A-28

US-09-817-198A-28

US-10-020-386-7830

US-10-020-386-7830
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                                                                                                                                                                                                                                                                                                                                                                                                                               4105333 seqs, 2784095677 residues
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GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                               December 24, 2004, 23:12:29
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Listing first 45 summaries
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Perfect score:
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13 534.2 16.4 566 9 US-09-764-868-507 Sequence 507, App Sequence 31, Appl 15 477.4 14.7 481 13 US-09-920-300.3 31. Sequence 303, App Sequence 1930, App Sequence 303, Ap
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Sequence 1, Application US/09817198A

Sequence 1, Application US/09817198A

Patent No. US20020146758A1

GENERAL INFORMATION:
APPLICANT: YE, Jane 1

TITLE OF INVENTION: RECTENS, AND USES THEREOF

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

TITLE OF INVENTION: PROTEINS

TITLE OF INVENTIONS

TITLE 
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100.0%; Pred. No. 0;
iive 0; Mismatches 0;
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Best Local Similarity
Matches 3257; Conserv
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3257
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CTGCAG 24	TGCAG 240  CATTIT 300  CATTIT 300  Db 1321	360 Db 1381	ATGAGG 420         Particular CCTTGCTTGCTTGCTTGCTCCGCCTGCCTGCTCTTTGGGGAACTGAGCTCAGAGGCAGGTGCTTCAG         Particular CCTTGCTTGGCTGCCCGCCTGCCTTTGGGGAACTGAGCTCAGAGGCAGGTGCTTCAG           ATGAGG 420         Db         1441         CCCTTGCTTGGCTGCCGCCTGCCTGTTTTGGGGAACTCAGAGGCAGGTGCTTCAG	SCATGG 480	STCTGA	CAGCA 600       CAGCA 600	GAACT	TTTCC 72	100H	0660T	CTTCA 90	37CTC 	GCTC 1	FTCTC 108	GTGT 	CCCAG 120	
GATGAAGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAGATCTGGGACAC 	GORGANIA CONTRACOS CALCARAS I COGAS INCAGATO I GGGARACO CONTRACA C	CTATGACATTAGCAGCGGGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACG	'IGATGAGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGG 	AGCAGAAACGGCAGGTGGGAAGAGAGCAAGGGCAGCAGCTGGCGAAGGAGTATGGC 		CAGAGCTGGTGCTGCAGGCCCATAGGAAGGAGGCTGGAAGGCCTCCGGATGCGTGCC 	ATGAGTTGGCACTGGCAGAGCTGGAGGAGGAGGGCAAACCCGAGGGCCCAGG 		CTCAGGAGGCCGTGGGCAGCAGGGAGCCGGGGCTTTGCCCTGCTGCTGTCTCT 	FIGATGACCCTATTGAGTATCAGTAGCCACTACTCCCCTGCCTG	FOT I	GCCTGTTTCCCCAGCCACAGGCCTGCTACGACCCCACGATGTGCCGCAAGCACTG 	ACCATCCGGCACCCACAGACAACAGCCAGGCTGGAGTCCAGGCCACTTTCAGCT 		9 9 9 9 9 9	ATGGA(	

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Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1782, Appl
Sequence 15247, A
Sequence 1552, Appli
Sequence 6, Appli
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110, Appl
142, App
142, App
646, App
11632, A
1422, Ap
1422, Ap
1422, Ap
1422, Ap
1423, Appli
6188, Ap
11843, A
11843, A
                                                           ; Search time 256 Seconds
(without alignments)
9043.123 Million cell updates/sec
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                                                                                                                        Sequence 16
Sequence 36
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Sequence
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'cgn2_6/ptodata/1/ina/5A_COMB.seq:*
'cgn2_6/ptodata/1/ina/5B_COMB.seq:*
'cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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'cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
'cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-300-958A-16

US-09-774-528-36

US-08-198-104-2

US-09-198-104-2

US-09-154-602-4

US-09-513-999C-1782

US-09-513-999C-1782

US-09-270-767-12624

US-09-270-767-12624

US-09-270-767-12624

US-09-270-767-12624

US-09-270-767-12624

US-09-270-767-12624

US-09-270-767-12624

US-09-270-767-12624

US-09-113-999C-1663

US-09-670-113-999C-16632

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US-09-620-312D-646

US-09-620-312D-646
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US-09-270-767-14743
US-09-270-767-1383
US-09-270-767-16665
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                                                                                                                                                                           824507 seqs, 355394441 residues
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Maximum Match 100%
Listing first 45 summaries
                                                             December 24, 2004, 18:57:48
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length: 2000000000
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174.2
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Perfect score:
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Sequence 1698, Application US/09513999C
; Sequence 1698, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Duclert, A.
; APPLICANT: Duclert, A.
; TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PATER REPRENCE: 59. US2. REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SEQ ID NO 1698
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                11701, F
66, Appl
28, Appl
1096, Ap
12890, A
37320, A
27320, A
2692, A
32591, A
                                                                                                                  989, App
1161, Ap
989, App
1161, Ap
989, App
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        Sequence Sequence
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Pred, No. 3e-45;
1; Mismatches 130;
US-09-248-796A-6190
US-09-620-312D-426
US-09-329-913-64
US-09-350-614-66
US-09-350-614-66
US-09-976-594-1096
US-09-976-594-1096
US-09-976-594-387
US-09-976-594-387
US-09-976-598-9
US-09-513-999C-2692
US-09-513-999C-2692
US-09-513-999C-2692
US-09-702-705-1161
US-09-702-705-1161
US-09-703-457-989
US-09-704-4124B-989
US-09-614-124B-989
                                                                                                                                                                                                    ALIGNMENTS
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Best Local Similarity 68.1%;
Matches 280; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORANISM: Homo sapiens
FEATURE:
I NAME/KEY: CDS
LOCATION: 29..412
FEATURE:
I NAME/KEY: misc_feature
LOCATION: 385
COTHER INFORMATION: y=c or t
US-09-513-999C-1698
  642
8333
7644
6399
9705
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1193
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   LENGTH: 412
   115.2
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APPLICANT:
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APPLICANT:
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Best Local S
Matches 288
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                 Sequence 16, Application US/09300958A

Patent No. 6495319

GRUERAL INFORMATION:
APPLICANT: Mcclelland, Michael
APPLICANT: Welsh, John
APPLICANT: Trankle, Thomas
ITILE OF INVENTION: Using Same
ITILE OF INVENTION: Using Same
FILE REFERENCE: P-PH 3457
CURRENT APPLICATION NUMBER: US/09/300,958A
CURRENT PILING DATE: 1999-04-27
FRIOR PELICATION NUMBER: 60/083,331
PRIOR FILING DATE: 1998-04-27
PRIOR PELICATION NUMBER: 60/098,070
PRIOR PELICATION NUMBER: 60/098,070
PRIOR PELICATION NUMBER: 60/118,624
FRIOR PELICATION NUMBER: 60/118,624
FRIOR PLING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PRECENTING USE: 2.0
SEQ ID NO 16
LENGTH: 730
                                                       317 CAGCGAGCGCTCTTACCAGCACATCATGAAGTGGGTCAGTGACGTGGATGAGTACGCACC 376
257 GACCATCACAAAGCAGTACTATCGGCGGGCCCAGGGGATATTTTGGTCTATGACATTAG 316
                        241 GACGATCACAACGGCCTACTACAGGGGTGCAATGGGCCATCATGCTGGTCTACGACATCAC 300
                                                                                 301 CAACGAGAAGTCCTTCGACAACATCCGGAACTGGATTCGCAACATTGAGGAGCACGCCTC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCACCGACAACGAGTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTAACATGA 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 AGACCATAGAGGTAGACGGCATCAAAGTGCGGATACAGATCTGGGACACTGCAGGGCAGG 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGACATTAGCAGCGAGGCGTCTTACCAGCACATCATGAAGTGGGGTCAGTGACGTGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 AGTACGCACCAGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGGAGCAGA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                404 AGAAC---TGTGATGATGATGCCGAATATTAGTGGGTAATAAGAATGACGACCCTGAGC 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACGGCAGGTGGGAAGAGGAAAGGGCAGCTGGCGAAGGAGGAGTATGGCATGGACTTCT 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                377 AGAAGGCGTCCAGAAGATCCTTATTGGGAATAAGGCTGATGAGGAGCAGAA 427
                                                                                                                                    3;
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Best Local Similarity 56.7%;
Matches 342; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                        RESULT 2
US-09-300-958A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: HOW
US-09-300-958A-16
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llarity 59.5%; Pred. No. 5.4e-33;
Conservative 0; Mismatches 193; Indels 3;
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TITLE OF INVENTION: No. 6743619e1 Nucleic Acids and
TITLE OF INVENTION: POlypeptides
FILE REFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: pt_FL_genes Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36, Application US/09774528
Patent No. 6743619
GENERAL INFORMATION:
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Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
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Ren, Feiyan
Zhang, Jie
Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
Wehrman, Tom
Wang, Jian-Rui
Wang, Dunrui
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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; LOCATION: (124)..(831)
US-09-774-528-36
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Genoscope.

AL Submission

AL Submission

AL Submission

AL Submitted (30-JAN-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fx)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and Cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

| Solution of Invitrogen | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Qualifiers | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Location/Collogies | Loc

source

FEATURES

Faraday Avenue 2 (bases 1 to 3151)

TITLE JOURNAL REFERENCE AUTHORS

COMMENT

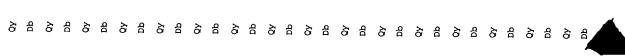
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/note="unnamed protein product"

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        Copyright
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- nucleic search, using sw model OM nucleic

December 24, 2004, 18:50:08; Search time 1459 Seconds (without alignments) 11718.550 Million cell updates/sec Run on:

US-09-817-198C-1 Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters: 4134886 segs, 2624710521 residues Searched:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_23Sep04:* Database

geneseqn1980s:* geneseqn1990s:* geneseqn2000s:*

geneseqn2003cs:* geneseqn2003ds:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* geneseqn2002as:* geneseqn2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aad47168 Human Ras Aa642285 Human imm Aad7165 Human Ras Aac75813 Human ORF Ab1440069 Human imm Ab134138 Human imm Ab27053 CDNA enco Ab23321 Human cDN Ad99321 Human cDN Ad993361 Human Dla Ad693748 Leukaemia Ac74635 Human Bla Ac74635 Human Bla Ac74635 Human Bla Ac74635 Human gen Ad693748 Leukaemia Ac7772 CDNA enco Ad693747 CDNA enco	Abl66992 Thyroid c Ach33636 Human end Adf81379 Leukaemia Aat25457 Human gen
SUMMARIES	AAD47168 AAAK82285 AAAK82285 AAAC75813 ABK40069 ABL34138 ABL34138 ABL34138 ABL34139 ABC3733 AAS27460 AAC2748 AAC2748 AAC37472 AAS27472 AAS27475	ABL66992 ACH33636 ADF81379 AAT25457
DB	8 4 8 8 8 8 8 8 8 8 8 8 8 9 9 9 9 9 9 9	9 6 7 7 7 7 9 9
% Query Match Length DB	3257 23240 28770 28770 7924 7924 7924 7924 7924 7924 7924 7924	463 458 410 320
% Query Match	100 82.0 82.0 82.0 33.0 33.0 33.0 33.0 33.0 33.0 33.0 3	13.5 13.0 11.8 9.6
Score	3257 2696.6 12696.6 1192.8 11192.8 1160.8 1160.0 1160.0 866.2 866.2 866.2 863.2 874.2	438.8 424.4 383 313.4
Result No.	0 00 00 00 00 00 00 00 00 00 00 00 00 0	c 18 19 20 21

Ab138341 Human col Ad24467 Human sof Ab409160 Human rab Ab45410 Human rab Ab45410 Human cova Ad168265 Human G-p Abv78060 Hypoxia-r Aas60884 Human can Aas60884 Human can Aas60898 Human can Aas60898 Human can Aas60897 Human pro Abv25781 Human pro Ad50076 Human hep Ad50770 Human hep Ad50770 Human hep Ad50770 Human nep Ad50771 Human sof Adb12721 Human sof Adb12721 Human sof	Adb52880 Primary r Aac01700 Human sec Aaa40104 Human Rab Aaa40108 Human Rab Aaa96887 Nucleotid
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# ALIGNMENTS

Human; Ras-like protein; inflammation; cell proliferation; apoptosis; immunodeficiency; neurodegenerative; Alzheimer's disease; cirrhosis; parkinson's disease; describing disease; cabexia; myocardial infarction; osteoporosis; atherosclerosis; glomerulonephritis; cohn's disease; irritable bowel syndrome; multiple sclerosis; osteoarthritis; allergy; pancreatitis; autoimmune thyroiditis; rheumatoid arthritis; osteopathic; Sjogren's syndrome; infection; transgenic; gene therapy; nootropic; gout; neuroprotective; vasotropic; cytostatic; dermatological; nephrotropic; ophthalmological; tranquilliser; cancer; stroke; Grave's disease; AIDS; asthma; anaemia; drug screening; gene; ss. Human Ras-like protein encoding cDNA. AAD47168 standard; cDNA; 3257 BP. (first entry) 24-FEB-2003 AAD47168; RESULT 1 AAD47168 

Homo sapiens

"Human Ras-like protein" Location/Qualifiers 45. .683 /*tag= b /product= "1 684. .3257 /*tag= c ø *tag= Key 5'UTR 3'UTR CDS

WO200277193-A2

03-OCT-2002

27-MAR-2002; 2002WO-US009328.

27-MAR-2001; 2001US-00817198.

(PEKE ) PE CORP.

Beasley EM; Ye J, Di Francesco V, Gan W,

2003-018913/01 WPI; 2003-018913/ P-PSDB; AAE29096 New isolated human Ras-like protein polypeptide, useful for diagnosing, treating or preventing inflammation and disorders associated with cell proliferation and apoptosis, e.g. AIDS, cancer, allergies, anemia, asthma stroke

Claim 4; Page 73-74; 82pp; English.

The invention relates to human Ras-like protein and its corresponding nucleic acid. The Ras-like protein and DNA is useful in the development of human therapetuics and diagnostic compositions. They are useful in the diagnosis, prevention and tagnostic compositions. They are useful in the associated with cell proliferation and apoptosis, e.g. AIDS and other infectious or genetic immunodeficiencies, neurodegenerative disease e.g. affections or genetic immunodeficiencies, neurodegenerative disease e.g. Alzheimer's disease, Parkinson's disease, wasting disease e.g. cachexia, is chaemic injuries e.g. myccardial infarction, stroke or reperfusion cirrhosis, osteoporosis or cancer. They are also used to treat disorders associated with inflammation including allergies, atopic dermatitis, catheroscierosis, asthma, anaemia, Crohn's disease, diabetes mellitus, C drave's disease, glomerulonephritis, gout, irritable bowel syndrome, cuvetis, trauma, or viral, bacterial, fungal, parasitic, protozoal or helminthic infections. The antibodies of the invention are useful in cuseful for studying the function of a Ras-like protein, and identifying and evaluating modulators of its activity. Ras-like protein is used in catheroscapenomic analysis or for tissue typing. The transgenic animals are constructed and evaluating modulators of its activity. Ras-like protein is used in gene therapy. The present

Sequence 3257 BP; 793 A; 892 C; 870 G; 702 T; 0 U; 0 Other;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

December 24, 2004, 18:56:50; Search time 13354 Seconds (without alignments) 11533.814 Million cell updates/sec Run on:

US-09-817-198C-1 3257 1 tgcccgctgcccgcag......aaaaaaaaaaaaaaaaa 3257 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4526729 seqs, 23644849745 residues Searched:

9053458 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

GenEmbl:* Database :

gb ba: *
gb brtg: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

co.	Description	BC040679 Homo sapi	AL139022 Human chr	BX640825 Homo sapi	AX347040 Seguence	AX348456 Sequence	AX347041 Sequence	AX348457 Seguence	AX399903 Sequence	BD205055 Human nuc	AX014147 Sequence	BC027769 Mus muscu	AX781147 Sequence	M83679 Sprague-Daw	CQ730386 Sequence	AX396088 Sequence	AX334820 Sequence	AC096084 Rattus no	BC013790 Mus muscu	AX779778 Sequence
SUMMARIES	Ð	BC040679	CNS01DX4	HSM806937	AX347040	AX348456	AX347041	AX348457	AX399903	BD205055	AX014147	BC027769	AX781147	RATRAB15X	CQ730386	AX396088	AX334820	AC096084	BC013790	AX779778
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	& Query Match	93.0	82.8	43.7	36.6	36.6	35.6	35.6	30.7	26.6	26.6	25.0	19.4	17.7	15.2	14.7	13.5	13.0	12.8	11.8
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# ALIGNMENTS

RESULT 1 BC040679 LOCUS DEFINITION	BC040679  Homo sapiens RAB15, member RAS onocogene family, mRNA (cDNA clone MGC:42319 IMAGE:4817835), complete cds.
VERSION KEYWORDS SOURCE ORGANISM	BC040679.2 GI:34783346 MGC. Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia: Butheria: Primates; Catarrhin; Hominidae; Homo.
REFERENCE AUTHORS	1 (bases 1 to 3326) Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Martusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
	Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
TITLE	DICKSOL, NO, KORTAGUEZ, A.C., STIMOGG, D., SCHMUCZ, J., MYETS, K.M., BUTTERTÍGEG Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and infitial analysis of more than 15,000 full-length himan and movies only sequences
JOURNAL PUBMED REFERENCE AUTHORS	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932 2 (bases 1 to 3326) Strausberg,R.
TITLE JOURNAL	Direct Submission Submitted (29-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

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Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Ghin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Telka Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 70 Row: p Column: 2.
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NIH-MGC Project URL: http://mgc.nci.nih.gov
On Sep 16, 2003 this sequence version replaced gi:26251822.
Contact: MGC help desk
Emmil: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tosh Library Preparation: Michael J. Brownstein (NHGRI) & Toshiyuki and Piero Carninci (RIREN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
EC Cancer Agency, Vancouver, BC, Canada
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95.8%; Pred. No. 0;
:ive 0; Mismatches 8; Indels 132;
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